(1) GENERAL INFORMATION:

    (i) APPLICANT: Jacobs, Kenneth
                   McCoy, John M.
                   Racie, Lisa A.
                   LaVallie, Edward R.
                   Merberg, David
                   Treacy, Maurice
                   Evans, Cheryl
                   Agostino, Michael
                   Lu, Zhijian
                   Honjo, Tasuku
                   Tashiro, Kei
                   Nakamura, Tomoyuki

    (ii) TITLE OF INVENTION: SECRETED PROTEINS

    (iii) NUMBER OF SEQUENCES: 2

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: Genetics Institute, Inc.
        (B) STREET: 87 CambridgePark Drive
        (C) CITY: Cambridge
        (D) STATE: MA
        (E) COUNTRY: U.S.A.
        (F) ZIP: 02140

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE:
        (C) CLASSIFICATION:

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Sprunger, Suzanne A.
        (B) REGISTRATION NUMBER: P-41,323

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (617) 498-8284
        (B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2362 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TAGCTTGGCA CGAGGGGACC CCGGCGCTCT CCCCGTGTCC TCTCCACGAC TCGCTCGGCC   60

CCTCTGGAAT AAAACACCCG CGAGCCCCGA GGGCCCAGAG GAGGCCGACG TGCCCGAGCT   120

CCTCCGGGGG TCCCGCCCGC GAGCTTTCTT CTCGCCTTCG CATCTCCTCC TCGCGCGTCT   180

TGGACATGCC AGGAATAAAA AGGATACTCA CTGTTACCAT TCTGGCTCTC TGTCTTCCAA   240

GCCCTGGGAA TGCACAGGCA CAGTGCACGA ATGGCTTTGA CCTGGATCGC CAGTCAGGAC   300

AGTGTTTAGA TATTGATGAA TGCCGAACCA TCCCCGAGGC CTGCCGAGGA GACATGATGT   360

GTGTTAACCA AAATGGCGGG TATTTATGCA TTCCCCGGAC AAACCCTGTG TATCGAGGGC   420

CCTACTCGAA CCCCTACTCG ACCCCCTACT CAGGTCCGTA CCCAGCAGCT GCCCCACCAC   480

TCTCAGCTCC AAACTATCCC ACGATCTCCA GGCCTCTTAT ATGCCGCTTT GGATACCAGA   540

TGGATGAAAG CAACCAATGT GTGGATGTGG ACGAGTGTGC AACAGATTCC CACCAGTGCA   600

ACCCCACCCA GATCTGCATC AATACTGAAG GCGGGTACAC CTGCTCCTGC ACCGACGGAT   660

ATTGGCTTCT GGAAGGCCAG TGCTTAGACA TTGATGAATG TCGCTATGGT TACTGCCAGC   720

AGCTCTGTGC GAATGTTCCT GGATCCTATT CTTGTACATG CAACCCTGGT TTTACCCTCA   780

ATGAGGATGG AAGGTCTTGC CAAGATGTGA ACGAGTGTGC CACCGAGAAC CCCTGCGTGC   840

AAACCTGCGT CAACACCTAC GGCTCTTTCA TCTGCCGCTG TGACCCAGGA TATGAACTTG   900

AGGAAGATGG CGTTCATTGC AGTGATATGG ACGAGTGCAG CTTCTCTGAG TTCCTCTGCC   960

AACATGAGTG TGTGAACCAG CCCGGCACAT ACTTCTGCTC CTGCCCTCCA GGCTACATCC 1020

TGCTGGATGA CAACCGAAGC TGCCAAGACA TCAACGAATG TGAGCACAGG AACCACACGT 1080

GCAACCTGCA GCAGACGTGC TACAATTTAC AAGGGGGCTT CAAATGCATC GACCCCATCC 1140

GCTGTGAGGA GCCTTATCTG AGGATCAGTG ATAACCGCTG TATGTGTCCT GCTGAGAACC 1200

CTGGCTGCAG AGACCAGCCC TTTACCATCT TGTACCGGGA CATGGACGTG GTGTCAGGAC 1260

GCTCCGTTCC CGCTGACATC TTCCAAATGC AAGCCACGAC CCGCTACCCT GGGGCCTATT 1320

ACATTTTCCA GATCAAATCT GGGAATGAGG GCAGAGAATT TTACATGCGG CAAACGGGCC 1380

CCATCAGTGC CACCCTGGTG ATGACACGCC CCATCAAAGG GCCCCGGGAA ATCCAGCTGG 1440

ACTTGGAAAT GATCACTGTC AACACTGTCA TCAACTTCAG AGGCAGCTCC GTGATCCGAC 1500

TGCGGATATA TGTGTCGCAG TACCCATTCT GAGCCTCGGG CTGGAGCCTC CGACGCTGCC 1560

TCTCATTGGC ACCAAGGGAC AGGAGAAGAG AGGAAATAAC AGAGAGAATG AGAGCGACAC 1620

AGACGTTAGG CATTTCCTGC TGAACGTTTC CCCGAAGAGT CAGCCCCGAC TTCCTGACTC 1680

TCACCTGTAC TATTGCAGAC CTGTCACCCT GCAGGACTTG CCACCCCCAG TTCCTATGAT 1740

ACAGTTATCA AAAAGTATTA TCATTGCTCC CCTGATAGAA GATTGTTGGT GAATTTTCAA 1800

GGCCTTCAGT TTATTTCCAC TATTTTCAAA GAAAATAGAT TAGGTTTGCG GGGGTCTGAG 1860

TCTATGTTCA AAGACTGTGA ACAGCTTGCT GTCACTTCTT CACCTCTTCC ACTCCTTCTC 1920

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TCACTGTGTT ACTGCTTTGC AAAGACCCGG GAGCTGGCGG GGAACCCTGG GAGTAGCTAG 1980

TTTGCTTTTT GCGTACACAG AGAAGGCTAT GTAAACAAAC CACAGCAGGA TCGAAGGGTT 2040

TTTAGAGAAT GTGTTTCAAA ACCATGCCTG GTATTTTCAA CCATAAAAGA AGTTTCAGTT 2100

GTCCTTAAAT TTGTATAACG GTTTAATTCT GTCTTGTTCA TTTTGAGTAT TTTTAAAAAA 2160

TATGTCGTAG AATTCCTTCG AAAGGCCTTC AGACACATGC TATGTTCTGT CTTCCCAAAC 2220

CCAGTCTCCT CTCCATTTTA GCCCAGTGTT TTCTTTGAGG ACCCCTTAAT CTTGCTTTCT 2280

TTAGAATTTT TACCCAATTG GATTGGAATG CAGAGGTCTC CAAACTGATT AAATATTTGA 2340

AGAGAAAAAA AAAAAAAAAA AA   2362

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 448 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Gly Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys
1   5   10   15

Leu Pro Ser Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp
            20   25   30

Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
        35   40   45

Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
        50   55   60

Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
65   70   75   80

Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
            85   90   95

Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile
            100   105   110

Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val
        115   120   125

Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
    130   135   140

Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
145   150   155   160

Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
                165   170   175

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Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
            180                 185                 190

Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val
        195                 200                 205

Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
    210                 215                 220

Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
225                 230                 235                 240

Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
            245                 250                 255

Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser
            260                 265                 270

Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
        275                 280                 285

Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr
    290                 295                 300

Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys
305                 310                 315                 320

Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala
            325                 330                 335

Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
        340                 345                 350

Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
        355                 360                 365

Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
    370                 375                 380

Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
385                 390                 395                 400

Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile
            405                 410                 415

Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
        420                 425                 430

Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
        435                 440                 445
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